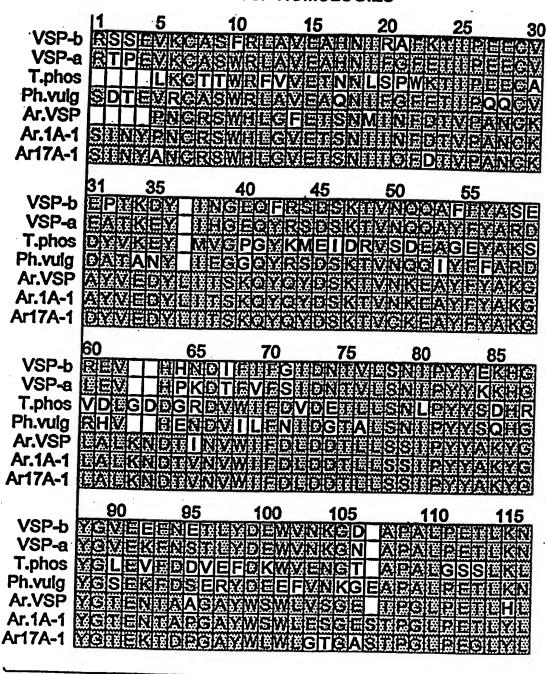




VSP HOMOLOGIES



TO FIG. 1B.

FIG. 1A.

2/9

FROM FIG. 1A

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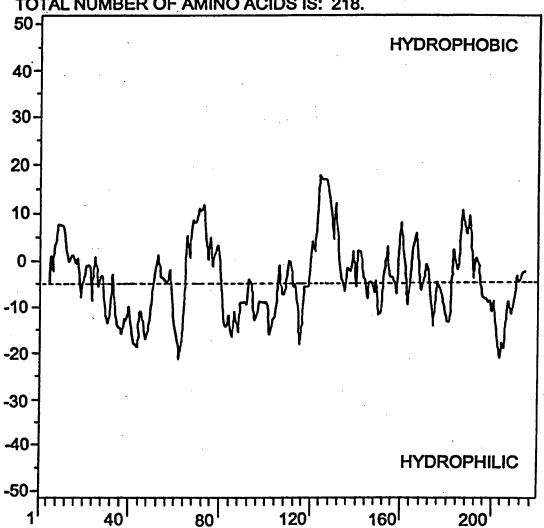
FROM FIG. 1A.									
MOD 6	CYPE TOP	120	12		130	13	35	140	145
VSP-b VSP-a	25 CA 10			KIEV				MAV	ANEK
		EVS		20 0 0 K	ESC			QAVT	ANNEK
Dh sada			EGY	NVF				RSVEY	
Ph.vulg Ar.VSP				**************************************					
Ar.1A-1									
Ar17A-1	YON		**************************************			1510	1212		
A IIA-I	APP.ULA		A STATE	en led kak	HEIGIY	[EVILL]	TOO TO	INIMIALI	LNEE
	1	50	155		160		165	170	175
VSP-b	KAG	通訊器	WEQ	#8 # [#]	संभावा		理智	VAILSY	
VSP-a	KAC	Ye his s	WEK	E88 E.	6 B E A	PS	22 E	MANSY	KTAA
T.phos	NAG	EH D	HK	EEEF	GSD	H	GK		KSER
Ph.vulg	KAG	YNI	YEK!	E	Joies	NS	AE	VVV	KTAE
Ar.VSP	AVG	VIK	MKHI	/HEK	PNG	KL	10	VVY	KSKV
		VIER						VVY	KSKV
Ar17A-1	AAG	YEY	NISIEI (BNG	SNE	RQ	VVY	KSKV
		400			400	1		-	
VSP-b	DEN	180	16 2000	35 55445225	190	PROPERTY	95	200	205
VSP-a		H L BY			16 16 A		901	EGD:	
Tinhos								LGSS	MC V
Ph.vulg	E A K					naw	NE	KGEN	
Ar.VSP	ANE				1616.5	now.		VEDE	
Ar.1A-1	RNS	VK	de la	T VE	NIE	DOW		VED:	
Ar17A-1	RNK	EVK	(GIV)	Ve	NIG	DOW	A TO	VED	
		210		21	3_				
VSP-b	REE	KREN	A B MA	XXXE					
		KER	~~~~~~~~	YIQ					
		KEP		XIL					
Ph.vulg	KSE	CLPK	IIEM X	YTK				•	
Ar.VSP	XIXIE			YVP	<u>S</u>				
		KLEN		XXX	S				
Ar17A-1	XXXXX		IIR LY	YVP.	S				

FIG. 1B.

PROPOSED VSPB METHIONINE-ENRICHED VARIANTS									
	11	5	10		15	20		. 25	30 EEQV
VSPB	RSS	EVKC	ASF	RLAV	EA	HNIR	AFK	TIP	EGV
VSPB-Met10		M				M			M
VSPB-Met20		M				M			M
VSPB-Met30		M				M		M	M
	31	35	40		45_	50		55	60
VSPA	EPT	KĎYII	NGFC	FRS	DSI	CTON	AQC		SERI
VSPB-Met10		M		M		<u> </u>			M
VSPB-Met20	М	M		M					M
VSPB-Met30	M	M		M		M			M
	61	65	70		7 5	80		85	90
VSPR	EMH	HNDI	FIFG			SNII	PYY		YGV
VSPB-Met10		M		M	M		· · · · · ·		
VSPB-Met20	M	M M		M	M				M
VSPB-Met30	M	M M		M	M	М			M
						440		445	
- 1/056	91	95	100	6 64116	105	110		115	120
MACO MACO	EEF	NETL	ADEM	VINK	GUP	MALI	<u> </u>	LKNI	NKL
VSPB-Met10				14					
VSPB-Met20 VSPB-Met30	- 14	M M		M	-		•		
VSPD-MBWU	M	M		IVI					
	121	125	130	1	35	140		145	150
		SFKI	VFLS	GRY	LDK		[EA		AGF
VSPB-Met10		M				M		M	
VSPB-Met20	M	M	M-		<u>M</u>	M		<u>M</u>	M
VSPB-Met30	M	M	M		M	<u>M</u>	M	M_	M
Part Table	151	155	160	1	65	170		175	180
	HTW		LKDP			IALSY	KS		
VSPB-Met10								M	M
VSPB-Met20				M		_M		M	M
VSPB-Met30			M	MM		M		<u>M</u>	<u>M</u>
	101	185	190	4	95	200		205	210
VSPA	ROGY	<u> 183</u> (R I V	जााँ द	WOO	SDL	LGDF	IRG	ESRT	FKL
VSPB-Met10	1140		M	<u> </u>		1-10	M		نا
VSPB-Met20			M			M	M	M	
VSPB-Met30			M			М	M	M	
	244	045 0	40						
Vepa	211 DND	215 2 /(YY 1	<u> 18</u>			 		·	
VSPB-Met10	PN PA		<u> </u>						
VSPB-Met20	N								
VSPB-Met30	<u> </u>						-		
		171							

FIG. 2.

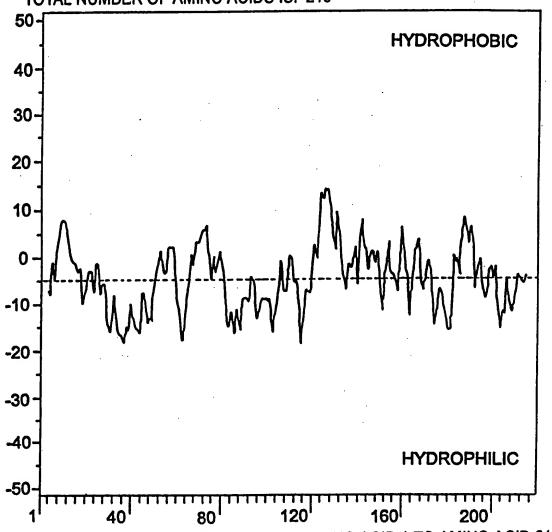
HYDROPATHY INDEX COMPUTATION FOR SEQUENCE VSPB. TOTAL NUMBER OF AMINO ACIDS IS: 218.



HYDROPATHIC INDEX OF VSPB FROM AMINO ACID 1 TO AMINO ACID 218. COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=-4.95).

FIG. 3A.

HYDROPATHY INDEX COMPUTATION FOR SEQUENCE VSPM10. TOTAL NUMBER OF AMINO ACIDS IS: 218



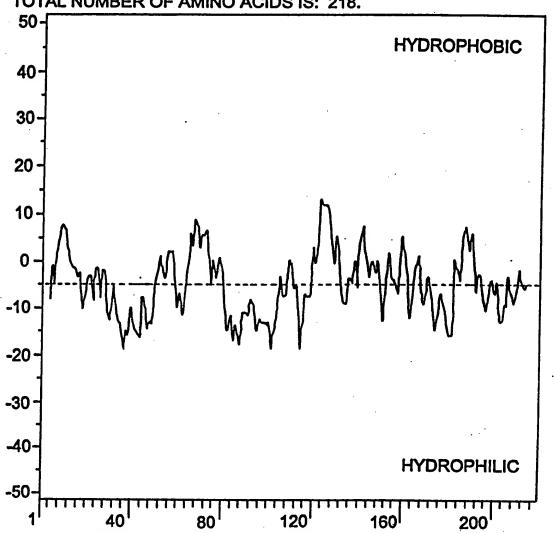
HYDROPATHIC INDEX OF VSPM1 FROM AMINO ACID 1 TO AMINO ACID 218. COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=5.52).

FIG. 3B.

Application No: 09/478,567 Amendment Dated: August 9, 2004 Reply to Office Action of April 8, 2004 REPLACEMENT SHEET

6/9

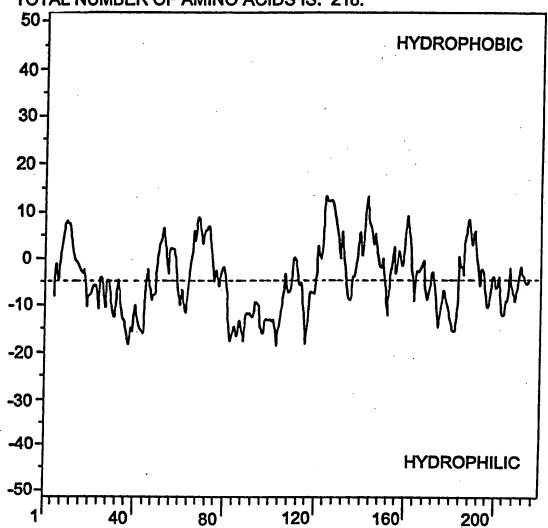




HYDROPATHIC INDEX OF VSPM20 FROM AMINO ACID 1 AMINO ACID 210. COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=-5.68).

FIG. 3C.

HYDROPATHY INDEX COMPUTATION FOR SEQUENCE VSPM30. TOTAL NUMBER OF AMINO ACIDS IS: 218.



HYDROPATHIC INDEX OF VSPM30 FROM AMINO ACID 1 TO AMINO ACID 218. COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=-5.31).

FIG. 3D.

VSPβ-met10 sequence

	<u>SfiI</u>	
1	GGCCCAGCCGGCCAGATCTTCGGAGATGAAATGCGCTAGCTTTAGGCTTGCTGTGGAAGC	60
	CCGGGTCGGCCGGTCTAGAAGCCTCTACTTTACGCGATCGAAATCCGAACGACACCTTCG	
61	<u>ACACAACATGCGAGCCTTTAAAACCATTCCTGAAGAGTGCATGGAACCAACAAAGGACTA</u>	120
	TGTGTTGTACGCTCGGAAATTTTGGTAAGGACTTCTCACGTACCTTGGTTGTTTCCTGAT	
121	CATGAATGGCGAACAATTTCGAATGGACTCTAAAACAGTTAACCAACAGGCCTTCTTTTA	180
	GTACTTACCGCTTGTTAAAGCTTACCTGAGATTTTGTCAATTGGTTGTCCGGAAGAAAAT	
181	TGCTAGTGAAATGGAAATGCATCACAACGACATGTTTATATTCGGCATGGATAACACCAT	240
	ACGATCACTTTACCTTTACGTAGTGTTGCTGTACAAATATAAGCCGTACCTATTGTGGTA	•
241	GCTCTCTAATATCCCATACTATGAAAAACATGGATATGGGGTGGAGGAATTTAATGAAAC	300
	CGAGAGATTATAGGGTATGATACTTTTTGTACCTATACCCCACCTCCTTAAATTACTTTG	
301	CTTATATGATGAATGGGTTAACAAGGGCGACGCACCGGCATTGCCAGAGACTCTTAAAAA	360
	GAATATACTACCCAATTGTTCCCGCTGCGTGGCCGTAACGGTCTCTGAGAATTTTT	
361	TTACAACAAGCTGATGTCCCTTGGCTTCAAGATGGTATTCTTGTCAGGAAGGTACCTTGA	420
	AATGTTGTTCGACTACAGGGAACCGAAGTTCTACCATAAGAACAGTCCTTCCATGGAACT	
421	CAAAATGGCCGTAACAGAAGCAAACCTAATGAAGGCTGGCT	480
	GTTTTACCGGCATTGTCTTCGTTTGGATTACTTCCGACCGA	
481	<u>AATTCTCAAGGATCCACATCTTATGACTCCAAATGCACTTTCATACAAATCAGCAATGAG</u>	540
	TTAAGAGTTCCTAGGTGTAGAATACTGAGGTTTACGTGAAAGTATGTTTAGTCGTTACTC	
541	<u>AGAGAATATGTTGAGGCAGGGATACAGAATTGTTGGAATGATTGGTGATCAATGGAGCGA</u>	600
	TCTCTTATACAACTCCGTCCCTATGTCTTAACAACCTTACTAACCACTAGTTACCTCGCT	
601	TCTGCTTGGAGACCACATGGGCGAATCTAGAACCTTTAAGCTTCCTAATCCCATGTACTA	660
	AGACGAACCTCTGGTGTACCCGCTTAGATCTTGGAAATTCGAAGGATTAGGGTACATGAT	
661	CATGGAGGCGGCCGC 675	
	GTACCTCCGCCGGCG	
	NotT	

COLONY LIFT ASSAY TO DETECT PROTEIN-PROTEIN INTERACTIONS

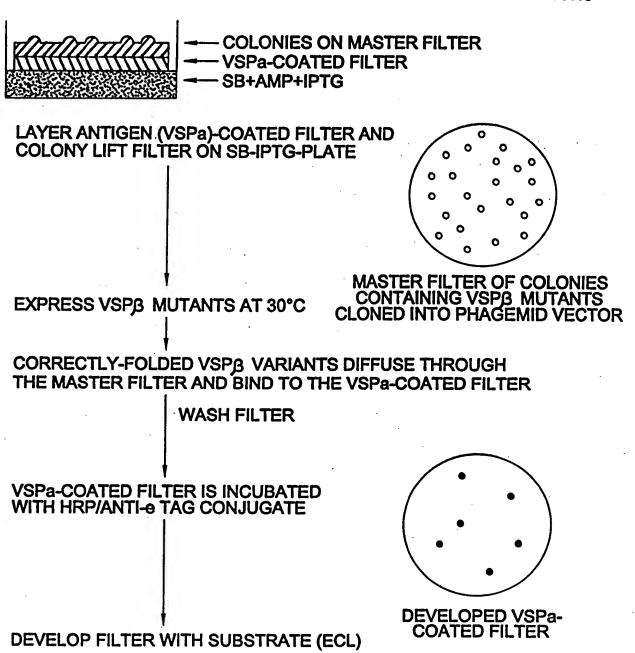


FIG. 5.